APPSA 2nd SCIENTIFIC CONFERENCE

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Diversification and phylogeny of *Fusarium* species complexes causing Soybean vascular wilts and root rot diseases in Lesotho

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Introduction

- Soybean - a major source of oil and proteins worldwide and the demand for soybean has increased in Africa
- Feed industry for poultry, aquaculture and home consumption (processed milk, baked beans and for blending with maize and wheat flour).
- Hence the introduction and promotion of Soybean in Lesotho
- High incidences of **foliar, root rot, stem and seed diseases**

Introduction Cont…..

- Plant diseases control depend on proper diagnosis of diseases and their causal agents.
- Disease control measures can be a waste of time and money - Without proper identification of the diseases
- Proper disease diagnosis is important to avoid plant losses
- Timely and effective disease management
- Becomes easier when associated with well-known symptoms

Introduction Cont…..

- Soybean root rot and wilting are the most worldwide soil-borne fungal diseases threatening soybean production.

- *Fusarium* is the most important causal agent of these diseases, causing large losses in soybean yield and quality

- More than 20 *Fusarium* species had been reported in different soybean-producing regions world-wide.

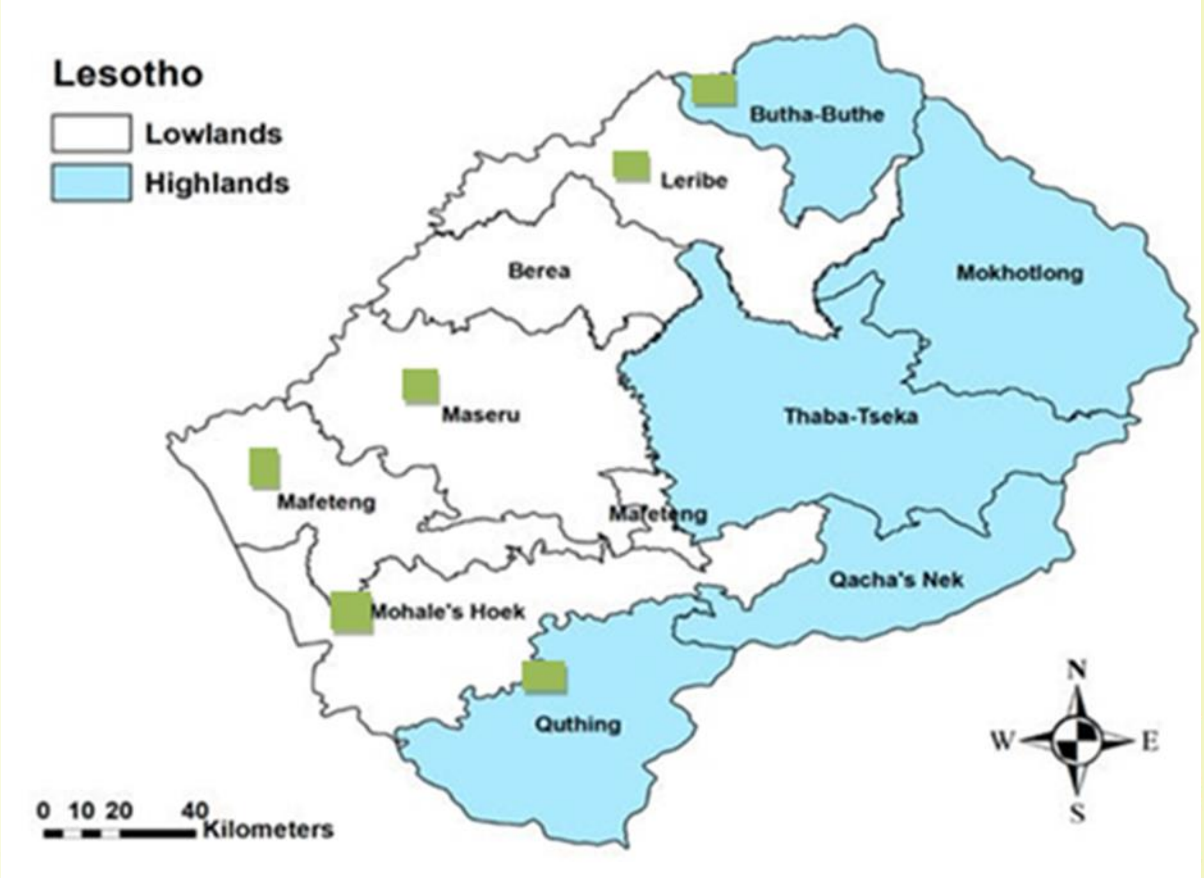
- *F. oxysporum* and *Neocosmospora solani* (formerly known as *Fusarium solani*) being the most predominant species

Objective

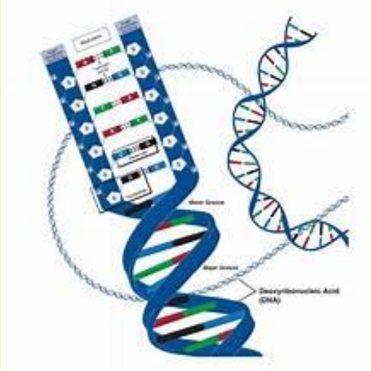
- To identify pathogens responsible for Soybean wilting and root rot through:
    - isolation of fungal microorganisms from symptomatic soybean stems, leaves and roots collected from five districts of Lesotho
    - identification of the isolates using classical and molecular-based methods
    - pathogenicity testing of *Fusarium* isolates to fulfil Koch's postulates.

Materials and Methods

- Soybean leaves and roots showing disease symptoms were collected from five districts of Lesotho planted with six Soybean cultivars in 2022 and 2023.



Materials and Methods



- Isolates were identified using colony morphological characterization of pure cultures on Potato Dextrose Agar (PDA)
- Molecular DNA sequencing of the internal transcribed spacer (ITS), elongation factor 1-alpha (TEF 1α) and the second subunit of RNA polymerase (RPB2) genes, using specific primers
- Phylogenetic analysis of the three genomic regions - Reference ITS sequences of *Fusarium* spp. retrieved from NCBI GenBank

Results

- Symptoms and Fungal Isolation

total of 20 fungal isolates were recovered from symptomatic soybean leaves and roots

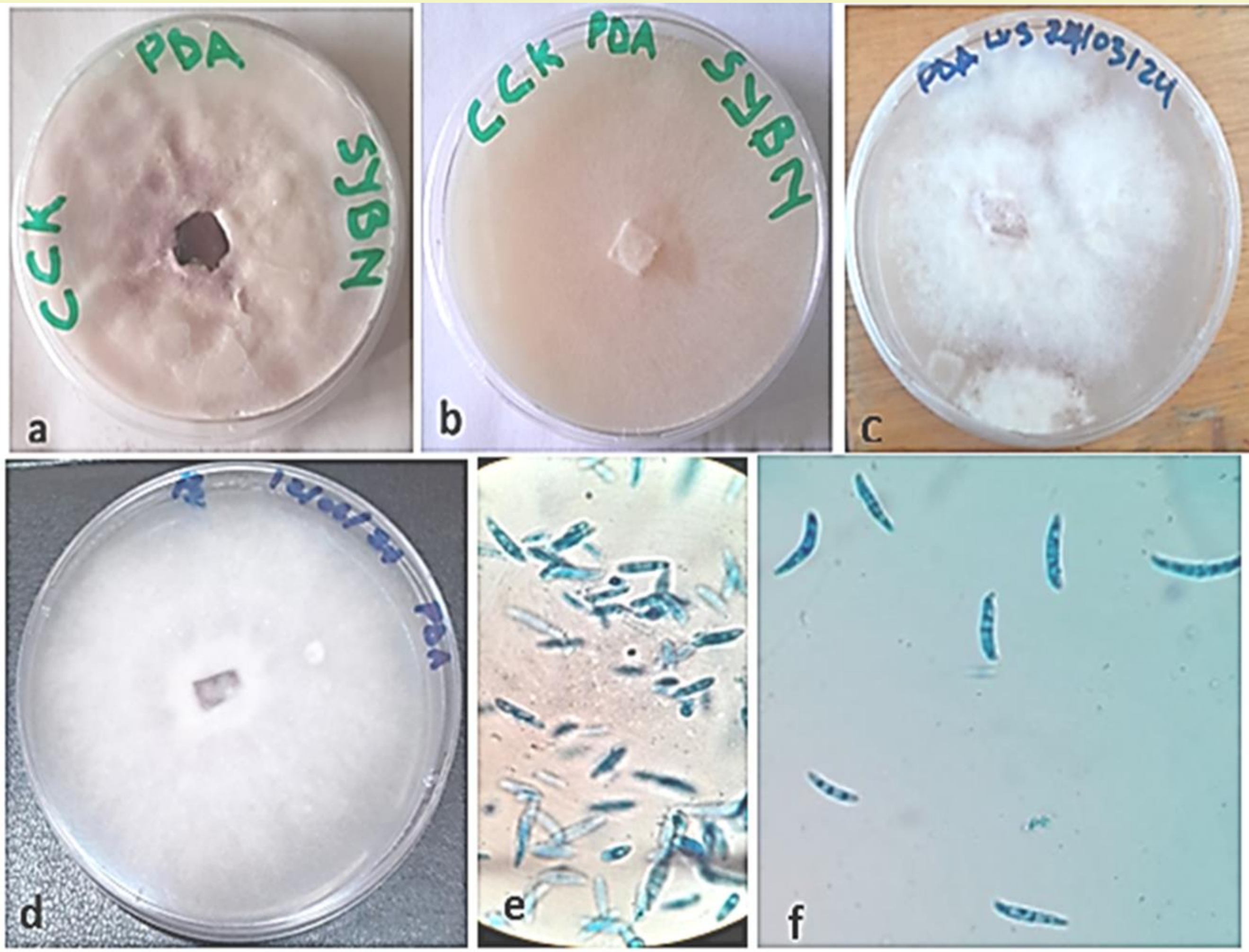
Morphological characterization revealed that *Fusarium* species were the most frequently isolated pathogens, constituting 75% of all isolates

Results…

- Colonies exhibited distinct white to pinkish-purple pigmentation with cottony mycelia

- morphological diversity in macroconidia and microconidia,

- variations in shape, size (ranging from 15–50 µm in length), and septation (0–5 septa per conidium)



Results….

- Molecular analyses confirmed two dominant representative species to be *Fusarium oxysporum* (30% of isolates) and N. solani (45% of isolates).

- These species were detected across all surveyed districts

- Non-pathogenic saprophytes, Mucor, Aspergillus, and Rhizopus, as well as known biocontrol agents such as *Trichoderma* spp.

Results….

- Morphologically distinct *Fusarium* isolates were selected for phylogenetic analysis.

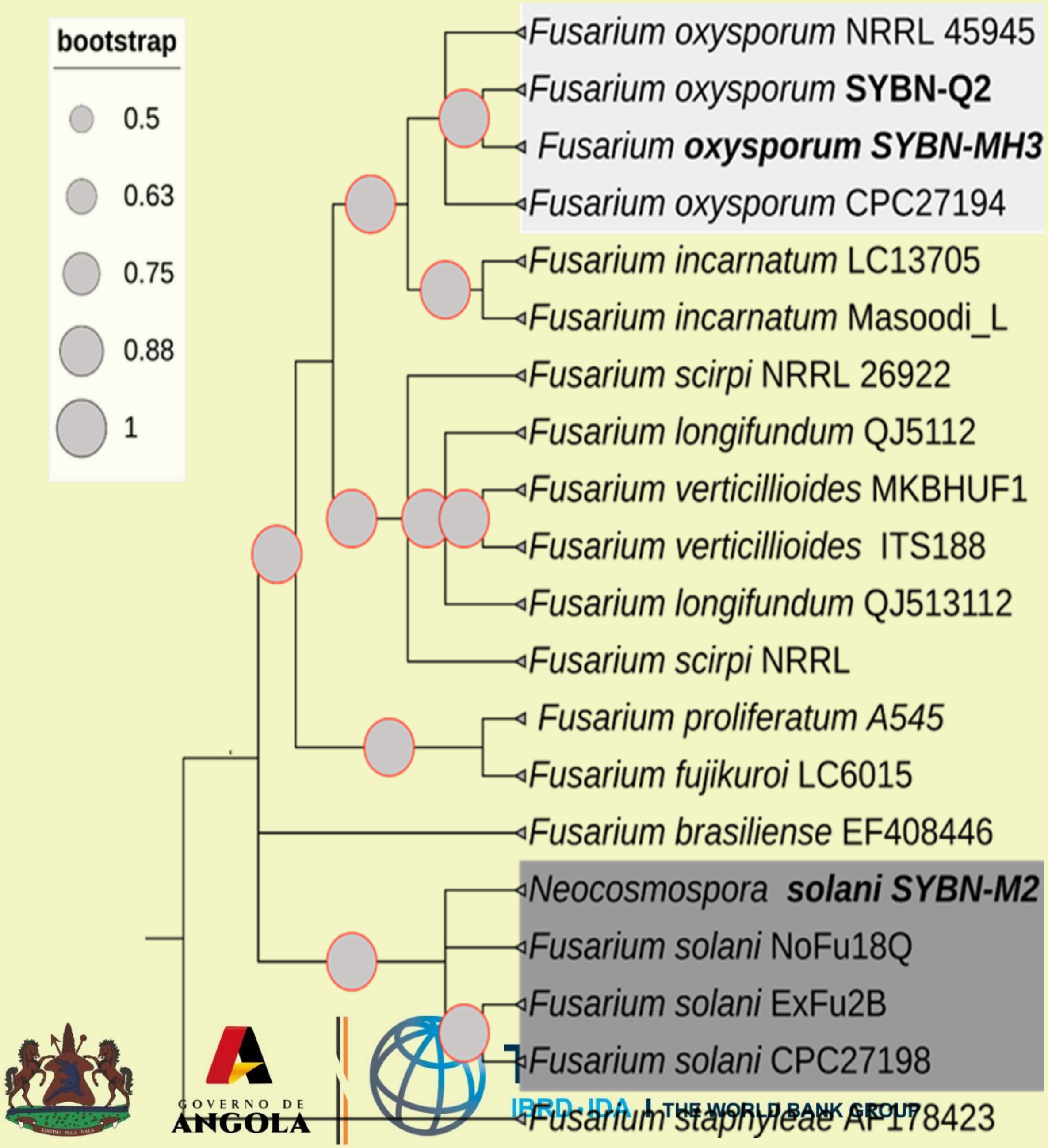
- Species identification was confirmed through BLASTn analysis of the ITS, TEF-1α, and RPB2

- New *Fusarium* sequences were deposited into NCBI GenBank databases

- will be used in future studies to understand the diversity of *Fusarium* spp. in Soybean and other crops.

Results…

- Sequences exhibited 99–100% identity with reference strains in both databases.
- Phylogenetic assignment, based on the highest sequence similarity matches, identified the isolates as *F. oxysporum* and *N. solani*.
- Phylogenetic tree - *F. oxysporum*, and *N. solani* isolates clustered with their corresponding *Fusarium* species from GenBank database with strong bootstrap values



Results…

- Pathogenicity test of *Fusarium species* confirmed that all 15 isolates were pathogenic, fulfilling Koch’s postulates

- Significant variation in aggressiveness was observed =

N. solani was the most aggressive species, with a mean disease severity index ranging from 72% to 82%.

- *F. oxysporum* species complex displayed variable pathogenicity, with severity indices between 17% and 61%, reflecting strain-specific differences

Conclusion

- This is the first documented report of these *Fusarium* species causing soybean diseases in Lesotho

- Understanding the diversity of pathogens is important in developing effective disease management strategies against diseases infecting soybean.

- Findings underscore the importance of integrating molecular diagnostics with pathogenicity assays

- To inform proper diagnoses of plant diseases, critical for mitigating yield and quality losses in soybean crops

Acknowledgements

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